

GenCore version 5.1.6
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OM nucleic - protein search, using .frame_plus_n2p model

Run on: August 22, 2003, 14:25:17 ; Search time 160 Seconds

(without alignments)
5009.446 Million cell updates/sec

Title: US-09-745-506-74

Sequence: 1 GCGATTGTTACTTGTGCTCTCTCTTACTTAACATTCGCA 1553

Scoring table:

OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 830525 seqs, 258052604 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1660916

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Command line parameters:

-MODE-frame_n2p.model -DEV-r1p
-Q/cgn2_1/USPTO.spool/US09745506/runat_22082003_132737_11185/app_query.fasta_1.1735
-DB-SPREMBL_23 -QFMT-fastan -SUFFIX-n2poli.rspt -MINMATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END-1 -MATRIX-oligo -TRANS-human40.cdi
-LIST-45 -DOCALLIGN-200 -THR_SCORE-quality -THR_MIN-1 -ALIGN-15 -MODE-LOCAL
-OUTFMT-pco -NORM-ext -HEAPSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09745506.eccn_1_1_223.grunat_22082003_132737_11185 -NCPU-6 -ICPU-3
-NO_MAP -LARGEBOILER -NEG_SCORES-0 -WAIT -DSBLOCK-100 -LONGLOG
-DEV_TIMEOUT-120 -WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-60 -XGAPEXT-60 -FGAPOP-6
-FGAPEXT-7 -YGAPOP-60 -YGAPEXT-60 -DELOP-6 -DELEXT-7

Database :

1: SPREMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	56	11.1	340	11 Q8C608 mus musculus

2	34	6.7	159	11	Q9D146	Q9D146 mus musculus
3	10	2.0	366	16	Q8NMB9	Q8NMB9 staphylococcus
4	10	2.0	366	16	Q8CSD9	Q8CSD9 staphylococcus
5	9	1.8	199	10	Q8LN76	Q8LN76 oryza sativa
6	9	1.8	334	16	Q8C4J3	Q8C4J3 bifidobacterium
7	9	1.8	415	16	Q8E5B2	Q8E5B2 streptococcus
8	9	1.8	575	5	Q8MZS4	Q8MZS4 physarum po
9	8	1.6	101	12	Q8UYE7	Q8UYE7 tt virus. o
10	8	1.6	108	16	Q8NMS2	Q8NMS2 corynebacter
11	8	1.6	109	10	Q8H7P1	Q8H7P1 oryza sativa
12	8	1.6	150	10	Q8H3B6	Q8H3B6 oryza sativa
13	8	1.6	151	5	Q61016	Q61016 crithidia f
14	8	1.6	208	4	Q8NH71	Q8NH71 homo sapien
15	8	1.6	211	15	Q9NAX0	Q9NAX0 feline immu
16	8	1.6	242	5	Q8SV52	Q8SV52 encephalito
17	8	1.6	248	5	Q9NED0	Q9NED0 leishmania
18	8	1.6	262	17	Q58376	Q58376 pyrococcus
19	8	1.6	262	17	Q8U233	Q8U233 pyrococcus
20	8	1.6	263	16	Q9L173	Q9L173 streptomyces
21	8	1.6	267	12	Q8V713	Q8V713 tt virus. o
22	8	1.6	277	12	Q8V712	Q8V712 tt virus. o
23	8	1.6	283	12	Q80851	Q80851 hydra angela m
24	8	1.6	309	16	Q9ZD99	Q9ZD99 rickettsia
25	8	1.6	309	16	Q9Z104	Q9Z104 rickettsia
26	8	1.6	311	16	Q8DLZ3	Q8DLZ3 synechococcus
27	8	1.6	312	16	Q9ZFB5	Q9ZFB5 listeria in
28	8	1.6	322	4	Q8NG11	Q8NG11 homo sapien
29	8	1.6	336	12	Q9DX57	Q9DX57 leek yellow
30	8	1.6	338	10	Q8RXK9	Q8RXK9 arabidopsis
31	8	1.6	346	4	Q8IU99	Q8IU99 homo sapien
32	8	1.6	355	2	Q05171	Q05171 streptomyces
33	8	1.6	367	11	Q9J119	Q9J119 rattus norv
34	8	1.6	367	11	Q9QNM6	Q9QNM6 mus musculu
35	8	1.6	369	2	Q9ANK6	Q9ANK6 bradyrhizob
36	8	1.6	368	10	Q9N906	Q9N906 arabidopsis
37	8	1.6	423	12	Q83108	Q83108 leek yellow
38	8	1.6	445	16	Q9KRL6	Q9KRL6 vibrio chol
39	8	1.6	449	16	Q98KY4	Q98KY4 rhizobium l
40	8	1.6	453	16	Q8CJ06	Q8CJ06 oceanobacill
41	8	1.6	458	16	Q8ECD1	Q8ECD1 shewanella
42	8	1.6	461	5	Q8IS43	Q8IS43 drosophila
43	8	1.6	466	5	Q9W5X8	Q9W5X8 drosophila
44	8	1.6	477	16	Q8P4S3	Q8P4S3 xanthomonas
45	8	1.6	478	10	Q9SUL4	Q9SUL4 arabidopsis

ALIGNMENTS

RESULT 1
ID Q8C608 PRELIMINARY; PRT; 340 AA.
AC Q8C608;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE N9gl Interacting factor 3-like 1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Testis;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL: AK076788; BAC36481.1; -
SQ SEQUENCE 340 AA; 37822 MW; 82DC63DB90B68B4E CRC64;

Alignment Scores:

Pred. No.: 4.7e-51 Length: 340
 Score: 56.00 Matches: 56
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 11.07% Indels: 0
 DB: 11 Gaps: 0

US-09-745-506-74 (1-1553) x Q8C608 (1-340)

OY 230 TCCTCCGCTTCCTGATGATTTGAGGCTCTCTCTTCTTCTGATGATTTGATTC 289
 |||||
 DB 22 SerSerArgSerPheMetAspLeuLysAlaLeuLeuSerSerLeuAsnAspPheAlaSer 41
 OY 290 CTCCTGTTTGTGAGAGTTGGGACATGTTGATTTACTGTGGAACCAAGCCACACAT 349
 |||||
 DB 42 LeuSerPheAlaGlnSerTrpAspAsnValGlyLeuLeuValGlnProSerProPheHis 61
 OY 350 ACCTGAATACACTCTCCGACCAATGACTGACTGAGAGATGATG 397
 |||||
 DB 62 ThrValAsnThrLeuPheLeuThrAsnAspLeuThrGlnValMet 77

RESULT 2

O9D146 PRELIMINARY: PRT: 159 AA.

AC O9D146: MEDLINE=21085660; PubMed=11217851;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 1110030624Rik protein.
 GN 1110030624Rik.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi S., Fukuda S.,
 RA Akawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Flieschmann W., Gaasterland T., Glissl C., King B., Kochiya H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nakado I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guattnich S., Hill D., Hofmann M., Hume D.A., Kamlya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Wittaker C., Wilmshut L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.,
 RA "Functional annotation of a full-length mouse cDNA collection";
 RT Nature 409:685-690(2001).
 DR EMBL: AK003978; BAB3102.1; -
 DR MGP: MGI:1913428; 1110030624Rik.
 DR InterPro: IPR002678; DUF34.
 DR Pfam: PF01784; DUF34; 1.
 SO SEQUENCE 159 AA; 17559 MW; FA8BCEB4FC165AC CRC64;

Alignment Scores:

Pred. No.: 3.97e-27 Length: 159
 Score: 34.00 Matches: 34
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 6.72% Indels: 0
 DB: 11 Gaps: 0

US-09-745-506-74 (1-1553) x Q9D146 (1-159)

OY 851 CAACTTATACGAAGACGGAAATTCGTGCTGAGAGACCTTCTTACATAGTGA 910
 |||||
 DB 12 GlnLeuYrGlnLysThrGlnLeuSerLeuGlnLysProLeuLeuHisThrGly 31
 OY 911 ATGGAGCGTTATGACACATGATGATTCCTCCCGGCA 952
 |||||
 DB 32 MetGlnArgLeuCysThrLeuAspGlnSerValSerLeuAla 45

RESULT 3

O8NMB9 PRELIMINARY: PRT: 366 AA.

AC O8NMB9: MEDLINE=22040717; PubMed=12044378;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein MM1511.
 GN MM1511.
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.,
 RT "Genome and virulence determinants of high virulence community-
 acquired MRSA.";
 RT Lancet 359:1819-1827(2002).
 RL EMBL: AP004827; BAB95376.1; -
 DR InterPro: IPR002678; DUF34; 1.
 DR Pfam: PF01784; DUF34; 1.
 DR TIGRFAMS: TIGR00486; TIGR00486; 1.
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 366 AA; 41153 MW; FA1F28762D878C79 CRC64;

Alignment Scores:

Pred. No.: 0.41 Length: 366
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.98% Indels: 0
 DB: 16 Gaps: 0

US-09-745-506-74 (1-1553) x Q8NMB9 (1-366)

OY 299 GCTGAGAGTGGACATGTTGATTTACTG 328
 |||||
 DB 19 AlaGlnSerTrpAspAsnValGlyLeuLeu 28

RESULT 4

O8CSD9 PRELIMINARY: PRT: 366 AA.

AC O8CSD9: MEDLINE=22040717; PubMed=12044378;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Conserved hypothetical protein.
 GN SE1246.
 OS Staphylococcus epidermidis.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1282;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12228;
 RA Zhang Y., Ren S., Li H., Fu G., Lu L., Lu G., Jia J., Tu Y., Qin Z.,
 RA Chen Z., Wen Y.,
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE016748; AA004845.1; -
 KW Hypothetical protein; Complete proteome.
 SO SEQUENCE 366 AA; 41639 MW; BF73A88EE77462A1 CRC64;

Alignment Scores:

Pred. No.: 0.41 Length: 366
 Score: 10.00 Matches: 10
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.98% RT Indels: 0
 DB: 16 Gaps: 0

US-09-745-506-74 (1-1553) x Q8CSD9 (1-366)

QY 299 GCTGAGAGTTGGACAAATGTTGATTCAG 328

DB 19 AAGlusterTrpaspasValGlyLeuLeu 28

RESULT 5

Q8LNT6 PRELIMINARY; PRT; 199 AA.

AC Q8LNT6; 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DE Hypothetical protein.

GN OSJNB0091N21.44.

OS Oryza sativa (japonica cultivar-group).

OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

OC Erihartoideae; Oryzaceae; Oryza.

OX NCBI_TaxID=39947;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Nipponbare;

RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.,

RA Overton II L.L., Bera J.J., Tsirlin T., Krol M.I., Jarrahl B.B.,

RA Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.B.,

RA Utterback T.T., Feldblum T.V., Yang Q.Q., Haas B.V., Suh B.B.,

RA Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.,

RT "Oryza sativa chromosome 10 BAC OSJNB0091N21 genomic sequence.";

RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC091122; AAM94932.1; -

DR Gramene; Q8LNT6; -

KW Hypothetical protein.

SQ SEQUENCE 199 AA; 21394 MW; 6C16C7C93AD3CFDC CRC64;

Alignment Scores:

Pred. No.: 5.37 Length: 199
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.78% RT Indels: 0
 DB: 10 Gaps: 0

US-09-745-506-74 (1-1553) x Q8LNT6 (1-199)

QY 732 ACGGTGTTCTGTCTACTCTTTTCG 758

DB 129 ThvAlpheleuSerleuLeuPheLeu 137

RESULT 6

Q8G4J3 PRELIMINARY; PRT; 334 AA.

AC Q8G4J3; 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DE Probable permease protein of ABC-transporter for peptides.

GN DPEC OR BL1389.

OS Bifidobacterium longum.

OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;

OC Bifidobacteriaceae; Bifidobacterium.

OX NCBI_TaxID=216816;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NCC 2705;

RX MEDLINE-22294977; PubMed-12381787;

RA Schell M.A., Karamitranzou M., Snel B., Vilanova D., Berger B.,

RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,

RA Pridmore R.D., Arigoni F.;

RT "The genome sequence of Bifidobacterium longum reflects its adaptation

to the human gastrointestinal tract.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).

DR EMBL; AE014768; AAN25188.1; -

KW Complete proteome.

SQ SEQUENCE 334 AA; 35667 MW; 646BEA878D670728 CRC64;

Alignment Scores:

Pred. No.: 5.05 Length: 334
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.78% RT Indels: 0
 DB: 16 Gaps: 0

US-09-745-506-74 (1-1553) x Q8G4J3 (1-334)

QY 1411 ATCAATTCGCGTTGTATCTTATTC 1437

DB 70 IleIleSerGlyLeuLeuLeuLeu 78

RESULT 7

Q8E5B2 PRELIMINARY; PRT; 415 AA.

AC Q8E5B2; 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DE Hypothetical protein.

GN G851120.

OS Streptococcus agalactiae (serotype III).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=216495;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=NEM316 / Serotype III;

RX MEDLINE-2242508; PubMed-12354221;

RA Glaser P., Rusniok C., Buchrieser C., Chevallier F., Frangeul L.,

RA Meadek T., Zouine M., Couve E., Lallou L., Poyart C., Tilleu-Cuot P.,

RA Kunst F.;

RT "Genome sequence of Streptococcus agalactiae, a pathogen causing

invasive neonatal disease.";

RL Mol. Microbiol. 45:1499-1513(2002).

DR EMBL; AL766848; CAD46779.1; -

DR Sagalst; qbs1120; -

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 415 AA; 47213 MW; 20029CB546FEA77F CRC64;

Alignment Scores:

Pred. No.: 4.91 Length: 415
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 1.78% RT Indels: 0
 DB: 16 Gaps: 0

US-09-745-506-74 (1-1553) x Q8E5B2 (1-415)

QY 1085 GGTGTTGAGCTGACCTTACCTCACA 1111

DB 176 GlyValGluAlaAspLeuTyrLeuThr 184

RESULT 8

ID Q8MZS4 PRELIMINARY; PRT; 575 AA.

AC Q8MZS4; 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Physaropepsin.
OS Physarum polycephalum (Slime mold).
OC Eukaryota; Mycetozoa; Myxogastromycetidae; Physarida;
OC Physarum.
OX NCBI_TaxID=5791;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NG-1;
RA Nishii W., Deki T., Miyashita R., Kim Y.-T., Sasaki N.,
Murakami-Murofushi K., Takahashi K.;
RT "Structural and enzymatic characterization of physaropepsin as a
RT unique serine-carboxyl proteinase.";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF502290; AA027198.1; -
DR InterPro: IPR000209; Peptidase_S8.
DR PROSITE: PS00138; SUBTILASE_SFR; 1.
SQ SEQUENCE 575 AA; 62708 MW; A538BD91E473BC5 CRC64;

Alignment Scores:

Pred. No.: 4.72 Length: 575
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.78% Indels: 0
DB: 5 Gaps: 0

US-09-745-506-74 (1-1553) x Q8MWS4 (1-575)

OY 741 CTGTCACTCTTTTTCCTAGGACTG 767

DB 4 LeuSerLeuLeuPheLeuGlyLeu 12

RESULT 9

O8UYE7 PRELIMINARY; PRT; 101 AA.

AC O8UYE7; 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORF2.
OS TT virus.
OC Viruses; ssDNA viruses; unclassified ssDNA viruses.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CT43F;
RX MEDLINE-21844401; PubMed-11855633;
RA Peng Y.H., Nishizawa T., Takahashi M., Ishikawa T., Yoshikawa A.,
Okamoto H.;
RT "Analysis of the complete genomes of thirteen TT virus variants
RT classifiable into the fourth and fifth genetic groups, isolated from
RT viremic infants.";
RL Arch. Virol. 147:21-41(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CT43F;
RA Okamoto H.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB064615; BAB79373.1; -
DR EMBL; AB064598; BAB79321.1; -
DR InterPro: IPR004118; TT_ORF2.
DR Pfam: PF02957; TT_ORF2; 1.
SQ SEQUENCE 101 AA; 10910 MW; 81E765F46826AC35 CRC64;

Alignment Scores:

Pred. No.: 71.1 Length: 101
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0
DB: 12 Gaps: 0

US-09-745-506-74 (1-1553) x Q8UYE7 (1-101)
OY 487 GAAGAGCGCCCTGATCGGAGC 510
DB 70 GluGlyAlaProGlyAspProGly 77

RESULT 10

Q8NMS2 PRELIMINARY; PRT; 108 AA.

AC Q8NMS2; 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical membrane protein Cg12493.
GN Cg12493.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP005281; BAB99886.1; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 108 AA; 12206 MW; 4C4D06AF9732F529 CRC64;

Alignment Scores:

Pred. No.: 70.6 Length: 108
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0
DB: 16 Gaps: 0

US-09-745-506-74 (1-1553) x Q8NMS2 (1-108)

OY 747 CTTCCTTTTCCTAGGACTGCTA 770

DB 15 LeuLeuPheLeuGlyLeuVal 22

RESULT 11

O8H7P1 PRELIMINARY; PRT; 109 AA.

AC O8H7P1; 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN OJ1217B09.5.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Sasaki C.,
Curtis J., Collura K.;
RA "Rice genomic Sequence.";
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC121489; AAN64139.1; -
KW Hypothetical protein.
SQ SEQUENCE 109 AA; 11673 MW; D0E4AAD20EDDF82A CRC64;

Alignment Scores:

Pred. No.: 70.5 Length: 109
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.58% Indels: 0

Alignment Scores:

Pred. No.:	65	length:	211
Score:	8.00	Matches:	8
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	1.61%	Indels:	0
DB:	15	Gaps:	0

US-09-745-506-74 (1-1553) x Q9WAX0 (1-211)

QY 408 AGCACTCTCTCATCACTCTCTCA 385

Db 193 SerThrSerSerIleThrSerSer 200

Search completed: August 22, 2003, 14:39:02
Job time : 166 secs